



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/803,580
Source: IFWO
Date Processed by STIC: 3/25/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<<http://www.uspto.gov/chc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313 1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/803,580

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION-SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 03/25/2004

PATENT APPLICATION: US/10/803,580

TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt

Output Set: N:\CRF4\03252004\J803580.raw

3 <110> APPLICANT: Syrrx, Inc.
 5 <120> TITLE OF INVENTION: HISTONE DEACETYLASE INHIBITORS
 7 <130> FILE REFERENCE: SYR-HDAC-5005-C2
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/803,580
 10 <141> CURRENT FILING DATE: 2004-03-17
 12 <150> PRIOR APPLICATION NUMBER: US 60/455,437
 13 <151> PRIOR FILING DATE: 2003-03-17
 15 <150> PRIOR APPLICATION NUMBER: US 60/531,203
 16 <151> PRIOR FILING DATE: 2003-12-19
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 513
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Custom
 28 <220> FEATURE:
W--> 29 <221> NAME/KEY: Residues 1-482 of HDAC1 and a 6-histidine tag at the N-terminus
 30 <222> LOCATION: (1)..(513)
 32 <400> SEQUENCE: 1

34	Met	Ser	Tyr	Tyr	His	His	His	His	His	His	Asp	Tyr	Asp	Ile	Pro	Thr
35	1				5						10				15	
38	Thr	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Ala	Met	Glu	Pro	Gly	Gly	Ser	Met
39			20						25					30		
42	Ala	Gln	Thr	Gln	Gly	Thr	Arg	Arg	Lys	Val	Cys	Tyr	Tyr	Tyr	Asp	Gly
43			35				40				45					
46	Asp	Val	Gly	Asn	Tyr	Tyr	Tyr	Gly	Gln	Gly	His	Pro	Met	Lys	Pro	His
47		50					55				60					
50	Arg	Ile	Arg	Met	Thr	His	Asn	Leu	Leu	Leu	Asn	Tyr	Gly	Leu	Tyr	Arg
51	65				70						75				80	
54	Lys	Met	Glu	Ile	Tyr	Arg	Pro	His	Lys	Ala	Asn	Ala	Glu	Glu	Met	Thr
55				85					90					95		
58	Lys	Tyr	His	Ser	Asp	Asp	Tyr	Ile	Lys	Phe	Leu	Arg	Ser	Ile	Arg	Pro
59				100					105					110		
62	Asp	Asn	Met	Ser	Glu	Tyr	Ser	Lys	Gln	Met	Gln	Arg	Phe	Asn	Val	Gly
63			115					120					125			
66	Glu	Asp	Cys	Pro	Val	Phe	Asp	Gly	Leu	Phe	Glu	Phe	Cys	Gln	Leu	Ser
67		130					135					140				
70	Thr	Gly	Gly	Ser	Val	Ala	Ser	Ala	Val	Lys	Leu	Asn	Lys	Gln	Gln	Thr
71	145				150						155				160	
74	Asp	Ile	Ala	Val	Asn	Trp	Ala	Gly	Gly	Leu	His	His	Ala	Lys	Lys	Ser
75				165				170						175		
78	Glu	Ala	Ser	Gly	Phe	Cys	Tyr	Val	Asn	Asp	Ile	Val	Leu	Ala	Ile	Leu
79				180					185						190	

Does Not Comply
 Corrected Diskette Needed
 (pg. 1-5)

Invalid (2137)
 Response

please see
 item # 10
 on error
 summary
 sheet.

RAW SEQUENCE LISTING

DATE: 03/25/2004

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TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt

Output Set: N:\CRF4\03252004\J803580.raw

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82 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
83      195      200      205
86 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
87      210      215      220
90 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
91 225      230      235      240
94 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
95      245      250      255
98 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
99      260      265      270
102 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
103      275      280      285
106 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
107      290      295      300
110 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
111 305      310      315      320
114 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr Ile
115      325      330      335
118 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
119      340      345      350
122 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
123      355      360      365
126 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
127      370      375      380
130 Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
131 385      390      395      400
134 Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
135      405      410      415
138 Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
139      420      425      430
142 Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
143      435      440      445
146 Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
147      450      455      460
150 Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
151 465      470      475      480
154 Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
155      485      490      495
158 Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
159      500      505      510

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162 Ala

166 <210> SEQ ID NO: 2

167 <211> LENGTH: 1542

168 <212> TYPE: DNA

169 <213> ORGANISM: Custom

172 <220> FEATURE:

W--> 173 <221> NAME/KEY: DNA sequence encoding residues 1-482 of HDAC1 and a 6-histidine
W--> 174 tag at the N-terminus
175 <222> LOCATION: (1)..(1542)

RAW SEQUENCE LISTING

DATE: 03/25/2004

PATENT APPLICATION: US/10/803,580

TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt

Output Set: N:\CRF4\03252004\J803580.raw

177 <400> SEQUENCE: 2

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178 atgtcgtact accatcacca tcaccatcac gattacgata tcccaacgac cgaaaacctg 60
180 tattttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg caccggagg 120
182 aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccacca 180
184 atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga 240
186 aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc 300
188 gatgactaca ttaaattctt gcgtccatc cgtccagata acatgtcgga gtacagcaag 360
190 cagatgcaga gattcaacgt tggtagaggac tgtccagtat tcgatggcct gtttgagttc 420
192 tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg 480
194 gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtcgga ggcattctggc 540
196 ttctgttacg tcaatgatata cgtcttgccc atcctggaac tgctaaagta tcaccagagg 600
198 gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaagaggc cttctacacc 660
200 acggaccggg tcatgactgt gtcctttcat aagtatggag agtacttccc aggaactggg 720
202 gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga 780
204 gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcatgtc caaagtaatg 840
206 gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat 900
208 cggttaggtt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgtcaag 960
210 agctttaacc tgcctatgct gatgctggga ggcggtggtt acaccattcg taacgttgcc 1020
212 cggtagctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca 1080
214 tacaatgact actttgaata ctttggaaca gatttcaagc tccacatcag tccttccaat 1140
216 atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac 1200
218 cttagaatgc tgccgcacgc acctggggtc caaatgcagg cgattcctga ggacgccatc 1260
220 cctgaggaga gtggcgatga ggacgaagac gacctgaca agcgcatctc gatctgctcc 1320
222 tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg 1380
224 ggccgcaaga actcttccaa cttcaaaaaa gccaaagagag tcaaaacaga ggatgaaaaa 1440
226 gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag 1500
228 ccagaagcca aaggggtcaa ggaggaggtc aagttggcct ga 1542

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231 <210> SEQ ID NO: 3

232 <211> LENGTH: 498

233 <212> TYPE: PRT

234 <213> ORGANISM: Custom

237 <220> FEATURE:

W--> 238 <221> NAME/KEY: Residues 1-488 of HDAC2 and a 6-histidine tag at the C-terminus

239 <222> LOCATION: (1)..(498)

241 <400> SEQUENCE: 3

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243 Met Gly Ser Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val Cys
244 1 5 10 15
247 Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
248 20 25 30
251 Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Asn
252 35 40 45
255 Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
256 50 55 60
259 Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
260 65 70 75 80
263 Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
264 85 90 95
267 Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
268 100 105 110

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RAW SEQUENCE LISTING

DATE: 03/25/2004

PATENT APPLICATION: US/10/803,580

TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt

Output Set: N:\CRF4\03252004\J803580.raw

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271 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
272      115      120      125
275 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
276      130      135      140
279 His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
280 145      150      155      160
283 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
284      165      170      175
287 Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
288      180      185      190
291 Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
292      195      200      205
295 Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
296      210      215      220
299 Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
300 225      230      235      240
303 Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
304      245      250      255
307 Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
308      260      265      270
311 Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
312      275      280      285
315 Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
316      290      295      300
319 Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
320 305      310      315      320
323 Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
324      325      330      335
327 Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
328      340      345      350
331 Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
332      355      360      365
335 Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
336      370      375      380
339 Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
340 385      390      395      400
343 Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
344      405      410      415
347 Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
348      420      425      430
351 Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
352      435      440      445
355 Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
356      450      455      460
359 Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
360 465      470      475      480
363 Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
364      485      490      495
367 His His

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RAW SEQUENCE LISTING

DATE: 03/25/2004

PATENT APPLICATION: US/10/803,580

TIME: 17:07:51

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt

Output Set: N:\CRF4\03252004\J803580.raw

371 <210> SEQ ID NO: 4
 372 <211> LENGTH: 1497
 373 <212> TYPE: DNA
 374 <213> ORGANISM: Custom
 377 <220> FEATURE:

W--> 378 <221> NAME/KEY: DNA sequence encoding residues 1-488 of HDAC2 and a 6-histidine
 W--> 379 tag at the C-terminus
 380 <222> LOCATION: (1)..(1497)
 382 <400> SEQUENCE: 4

383	atgggatcca	tggcgtacag	tcaaggaggc	ggcaaaaaaa	aagtctgcta	ctactacgac	60
385	ggtgatattg	gaaattatta	ttatggacag	ggtcatccca	tgaagcctca	tagaatccgc	120
387	atgaccata	acttgctgtt	aaattatggc	ttatacagaa	aaatggaaat	atataggccc	180
389	cataaagcca	ctgccgaaga	aatgacaaaa	tatcacagtg	atgagtatat	caaatttcta	240
391	cggatcaata	gaccagataa	catgtctgag	tatagtaagc	agatgcagag	atttaagtgt	300
393	ggagaagatt	gtccagtgtt	tgatggactc	tttgagtttt	gtcagctctc	aactggcggt	360
395	tcagttgctg	gagctgtgaa	gttaaaccga	caacagactg	atatggctgt	taattgggct	420
397	ggaggattac	atcatgctaa	gaaatcagaa	gcatacaggat	tctgttacgt	taatgatatt	480
399	gtgcttgcca	tccttgaatt	actaaagtat	catcagagag	tcttatatat	tgatatagat	540
401	attcatcatg	gtgatggtgt	tgaagaagct	ttttatacaa	cagatcgtgt	aatgacggtg	600
403	tcattccata	aatatgggga	atactttcct	ggcacaggag	acttgaggga	tattggtgct	660
405	ggaaaaggca	aatactatgc	tgtcaatttt	ccaatgagag	atggtataga	tgatgagtca	720
407	tatgggcaga	tatttaagcc	tattatctca	aaggtgatgg	agatgtatca	acctagtgt	780
409	gtggtattac	agtgtggtgc	agactcatta	tctggtgata	gactgggttg	tttcaatcta	840
411	acagtcaaag	gtcatgctaa	atgtgtagaa	gttgtaaaaa	cttttaactt	accattactg	900
413	atgcttgagg	gaggtggcta	cacaatccgt	aatgttgctc	gatgttgac	atatgagact	960
415	gcagttgccc	ttgattgtga	gattcccaat	gagttgccat	ataatgatta	ctttgagtat	1020
417	tttggaccag	acttcaaact	gcatattagt	ccttcaaaca	tgacaaacca	gaacactcca	1080
419	gaatatatgg	aaaagataaa	acagcgtttg	tttgaaaatt	tgcgcatgtt	acctcatgca	1140
421	cctggtgtcc	agatgcaagc	tattccagaa	gatgctgttc	atgaagacag	tggagatgaa	1200
423	gatggagaag	atccagacaa	gagaatttct	attcgagcat	cagacaagcg	gatagcttgt	1260
425	gatgaagaat	tctcagattc	tgaggatgaa	ggagaaggag	gtcgaagaaa	tgtggctgat	1320
427	cataagaaag	gagcaaagaa	agctagaatt	gaagaagata	agaaagaaac	agaggacaaa	1380
429	aaaacagacg	ttaaggaaga	agataaatcc	aaggacaaca	gtggtgaaaa	aacagatacc	1440
431	aaaggaacca	aatcagaaca	gctcagcaac	cccgggcatc	accatcacca	tcactaa	1497

434 <210> SEQ ID NO: 5
 435 <211> LENGTH: 782
 436 <212> TYPE: PRT
 437 <213> ORGANISM: Custom
 440 <220> FEATURE:

W--> 441 <221> NAME/KEY: Residues 73-845 of HDAC6 and a 6-histidine tag at the C-terminus
 442 <222> LOCATION: (1)..(782)
 444 <400> SEQUENCE: 5

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447	1			5					10						15	
450	Gly	Leu	Val	Leu	Asp	Glu	Gln	Leu	Asn	Glu	Phe	His	Cys	Leu	Trp	Asp
451				20					25						30	
454	Asp	Ser	Phe	Pro	Glu	Gly	Pro	Glu	Arg	Leu	His	Ala	Ile	Lys	Glu	Gln
455				35					40						45	
458	Leu	Ile	Gln	Glu	Gly	Leu	Leu	Asp	Arg	Cys	Val	Ser	Phe	Gln	Ala	Arg

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

VERIFICATION SUMMARY

DATE: 03/25/2004

PATENT APPLICATION: US/10/803,580

TIME: 17:07:52

Input Set : A:\SYR-HDAC-5005-C2.ST25.txt

Output Set: N:\CRF4\03252004\J803580.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:173 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:174 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:2
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:378 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:379 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4
L:441 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:650 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:6
L:742 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:854 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:855 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:8